IN THE CLAIMS:

Please cancel claim 39 without prejudice to applicants' prosecuting this claim, or claims of similar scope, in one or more continuation applications.

Please amend claims 25, 26, 32, 50, 51, 52, 57, 58, 72 and 75 to read as follows.

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25 (once amended). A method of targeted sequence alteration of a nucleic acid, comprising:

combining the targeted nucleic acid, in the presence of cellular repair proteins present within selectively enriched cells, cells in culture, or cell-free extracts, with a single-stranded oligonucleotide 17 - 121 nucleotides in length, said oligonucleotide having an internally unduplexed domain of at least 8 contiguous deoxyribonucleotides,

wherein said oligonucleotide is fully complementary in sequence to the sequence of a first strand of the nucleic acid target, but for one or more mismatches as between the sequences of said internally unduplexed deoxyribonucleotide domain and its complement on said target nucleic acid first strand, each of said mismatches positioned at least 8 nucleotides from said oligonucleotide's 5' and 3' termini, and

wherein said oligonucleotide has at least one terminal modification selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages.

26 (once amended). The method of claim 25, wherein said sequence alteration is a substitution of at least one base.

32 (once amended). The method of claim 31, wherein said genomic DNA is in a chromosome.

50 (once amended). The method of claim 49, wherein said human cell is selected from the group consisting of liver cell, lung cell, colon cell, cervical cell, kidney cell, epithelial cell, cancer cell, and stem cell.

51 (once amended). The method of claim 45, wherein said eukaryotic cell is from a mammal.

52 (once amended). The method of claim 51, wherein said mammal is selected from the group consisting of: rodent, mouse, hamster, rat, and monkey.

57 (once amended). The method of claim 25, wherein the sequences of said internally unduplexed deoxyribonucleotide domain and of the target nucleic acid first strand are mismatched at a single nucleotide.

58 (once amended). The method of claim 25, wherein the sequences of said internally unduplexed deoxyribonucleotide domain

and of its complement on the target nucleic acid first strand are mismatched at two or more nucleotides.

72 (once amended). The method of claim 71, wherein said human beta-globin gene is targeted in a human hematopoietic stem cell.

75 (once amended). A method of targeted sequence alteration of a nucleic acid, comprising:

combining the targeted nucleic acid, in the presence of cellular repair proteins present within selectively enriched cells, cells in culture, or cell-free extracts, with a single-stranded oligonucleotide 17 - 121 nucleotides in length, said oligonucleotide having an internally unduplexed domain of at least 8 contiguous deoxyribonucleotides,

wherein said oligonucleotide is fully complementary in sequence to the sequence of a first strand of the nucleic acid target, but for one or more mismatches as between the sequences of said internally unduplexed deoxyribonucleotide domain and its complement on said target nucleic acid first strand, each of said mismatches positioned at least 8 nucleotides from said oligonucleotide's 5' and 3' termini, and

wherein said oligonucleotide has at least one terminal modification and includes the sequence of any one of SEQ ID NOs: 1 - 4340.